SEQUENCE LISTING

SEQ ID NO: 1 is mouse TECK nucleotide sequence.
SEQ ID NO: 2 is mouse TECK amino acid sequence.
SEQ ID NO: 3 is human TECK nucleotide sequence.
SEQ ID NO: 4 is human TECK amino acid sequence.
SEQ ID NO: 5 is human MIP-3α nucleotide sequence.
SEQ ID NO: 6 is human MIP-3α amino acid sequence.
SEQ ID NO: 7 is human MIP-3β nucleotide sequence.
SEQ ID NO: 8 is human MIP-3β amino acid sequence.
SEQ ID NO: 9 is human DC CR nucleotide sequence.
SEQ ID NO: 10 is human DC CR amino acid sequence.
SEQ ID NO: 11 is human M/DC CR nucleotide sequence.
SEQ ID NO: 12 is human M/DC CR amino acid sequence.
SEQ ID NO: 13 is human CCKR1 amino acid sequence.
SEQ ID NO: 14 is human CCKR2 amino acid sequence.
SEQ ID NO: 15 is human CCKR3 amino acid sequence.
SEQ ID NO: 16 is human CCKR4 amino acid sequence.
SEQ ID NO: 17 is HPRT sense primer.
SEQ ID NO: 18 is HPRT antisense primer.
SEQ ID NO: 19 is FLAG epitope tag sequence.
SEQ ID NO: 20 is TECK sense primer
SEQ ID NO: 21 is TECK antisense primer
SEQ ID NO: 22 is exon 1-specific CRAM primer
SEQ ID NO: 23 is exon 2-specific CRAM primer
SEQ ID NO: 24 is exon 3-specific CRAM primer
SEQ ID NO: 25 is CRAM primer
SEQ ID NO: 26 is CRAM primer

<110> Wang, Wei

Gish, Kurt C.

Schall, Thomas J.

Vicari, Alain P.

Zlotnik, Albert

<120> Methods for using chemokine TECK

<130> DX0589K1D US

<150> US 10/039,659

<151> 2002-01-03

<150> US 08/887,977

<151> 1997-07-03

<150> US 60/021,664

<151> 1996-07-05

<150> US 60/028,329

<151> 1996-10-11

<150> US 60/048,593

<151> 1997-06-04

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tcaggtatct ggagaggaga tctaaccttc act atg aaa ctg tgg ctt ttt gcc     114
                                       Met Lys Leu Trp Leu Phe Ala
                                       1               5

tgc ctg gtt gcc tgt ttt gtt ggg gcc tgg atg ccg gtt gtc cat gcc     162
Cys Leu Val Ala Cys Phe Val Gly Ala Trp Met Pro Val Val His Ala
        10                  15                  20

caa ggt gcc ttt gaa gac tgc tgc ctg ggt tac cag cac agg atc aaa     210
Gln Gly Ala Phe Glu Asp Cys Cys Leu Gly Tyr Gln His Arg Ile Lys
    25                  30                  35

tgg aat gtt ctc cgg cat gct agg aat tat cac cag cag gaa gtg agt     258
Trp Asn Val Leu Arg His Ala Arg Asn Tyr His Gln Gln Glu Val Ser
40                  45                  50                  55

gga agc tgc aac cta cgt gct gtg aga ttc tac ttc cgc cag aaa gta     306
Gly Ser Cys Asn Leu Arg Ala Val Arg Phe Tyr Phe Arg Gln Lys Val
                60                  65                  70

gtg tgt ggg aat cca gag gac atg aat gtg aag agg gcg ata aga atc     354
Val Cys Gly Asn Pro Glu Asp Met Asn Val Lys Arg Ala Ile Arg Ile
            75                  80                  85

ttg aca gct agg aaa agg cta gtc cac tgg aag agc gcc tca gac tct     402
Leu Thr Ala Arg Lys Arg Leu Val His Trp Lys Ser Ala Ser Asp Ser
        90                  95                  100

cag act gaa agg aag aag tca aac cat atg aag tcc aag gtg gag aac     450
Gln Thr Glu Arg Lys Lys Ser Asn His Met Lys Ser Lys Val Glu Asn
    105                 110                 115

ccc aac agt aca agc gtg agg agt gcc acc cta ggt cat ccc agg atg     498
Pro Asn Ser Thr Ser Val Arg Ser Ala Thr Leu Gly His Pro Arg Met
120                 125                 130                 135

gtg atg atg ccc aga aag acc aac aat taagttaatt actcagagta           545
Val Met Met Pro Arg Lys Thr Asn Asn
                140

agcaccagct ggaggatggg cggagtctgc tgaagtgctg tcttctaggc atgccagtgc   605

caatgaactc actgaagcta cagtttcctg tacaagacca gacccaccaa cgtctcagca   665

tgtacgagga aggaactact gcgctaaagg ccctcccact caccaaggag ctattggcta   725

ttgatgattg ctgagggaag ggagtaattt tttttctctt tctgaagtgt gacttgagta   785

aattgcccat agttcagtat ataatcccca acctgtgctc aggcaagcaa ccctaattaa   845

atgcaatagc cacatacaaa agaagaggat atgaatagtt tggtaggagg ggcttgttag   905

gaagaagaca ttaacaggag agagaggagc gagaggatag tgagtgtgtg agagtgcctg   965

cacgtgtgaa atggtcaaag aattaaaaaa taaaaactta aaaagctatt aaaaagtaaa  1025
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Trp Met Pro Val Val His Ala Gln Gly Ala Phe Glu Asp Cys Cys Leu
20 25 30

Gly Tyr Gln His Arg Ile Lys Trp Asn Val Leu Arg His Ala Arg Asn
35 40 45

Tyr His Gln Gln Glu Val Ser Gly Ser Cys Asn Leu Arg Ala Val Arg
50 55 60

Phe Tyr Phe Arg Gln Lys Val Val Cys Gly Asn Pro Glu Asp Met Asn
65 70 75 80

Val Lys Arg Ala Ile Arg Ile Leu Thr Ala Arg Lys Arg Leu Val His
85 90 95

Trp Lys Ser Ala Ser Asp Ser Gln Thr Glu Arg Lys Lys Ser Asn His
100 105 110

Met Lys Ser Lys Val Glu Asn Pro Asn Ser Thr Ser Val Arg Ser Ala
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atatcggtgg ccccgttatt cgtccaggtg cccagggagg aggacccgcc tgcagc atg      119
                                                                  Met

aac ctg tgg ctc ctg gcc tgc ctg gtg gcc ggc ttc ctg gga gcc tgg      167
Asn Leu Trp Leu Leu Ala Cys Leu Val Ala Gly Phe Leu Gly Ala Trp
        -20                 -15                 -10

gcc ccc gct gtc cac acc caa ggt gtc ttt gag gac tgc tgc ctg gcc      215
Ala Pro Ala Val His Thr Gln Gly Val Phe Glu Asp Cys Cys Leu Ala
    -5              -1  1               5                   10

tac cac tac ccc att ggg tgg gct gtg ctc cgg cgc gcc tgg act tac      263
Tyr His Tyr Pro Ile Gly Trp Ala Val Leu Arg Arg Ala Trp Thr Tyr
                15                  20                  25

cgg atc cag gag gtg agc ggg agc tgc aat ctg cct gct gcg ata ttc      311
Arg Ile Gln Glu Val Ser Gly Ser Cys Asn Leu Pro Ala Ala Ile Phe
            30                  35                  40

tac ctc ccc aag aga cac agg aag gtg tgt ggg aac ccc aaa agc agg      359
Tyr Leu Pro Lys Arg His Arg Lys Val Cys Gly Asn Pro Lys Ser Arg
        45                  50                  55

gag gtg cag aga gcc atg aag ctc ctg gat gct cga aat aag gtt ttt      407
Glu Val Gln Arg Ala Met Lys Leu Leu Asp Ala Arg Asn Lys Val Phe
    60                  65                  70
```

```
gca aag ctc cac cac aac atg cag acc ttc caa gca ggc cct cat gct      455
Ala Lys Leu His His Asn Met Gln Thr Phe Gln Ala Gly Pro His Ala
75                  80                  85                  90

gta aag aag ttg agt tct gga aac tcc aag tta tca tca tcc aag ttt      503
Val Lys Lys Leu Ser Ser Gly Asn Ser Lys Leu Ser Ser Ser Lys Phe
                95                  100                 105

agc aat ccc atc agc agc agc aag agg aat gtc tcc ctc ctg ata tca      551
Ser Asn Pro Ile Ser Ser Ser Lys Arg Asn Val Ser Leu Leu Ile Ser
            110                 115                 120

gct aat tca gga ctg tgagccggct catttctggg ctccatcggc acaggagggg      606
Ala Asn Ser Gly Leu
        125

ccggatcttt ctccgataaa accgtcgccc tacagaccca gctgtcccca cgcctctgtc    666

ttttgggtca agtcttaatc cctgcacctg agttggtcct ccctctgcac ccccaccacc    726

tcctgcccgt ctggcaactg gaaagaagga gttggcctga ttttaacctt ttgccgctcc    786

ggggaacagc acaatcctgg gcagccagtg gctcttgtag agaaaactta ggatacctct    846

ctcactttct gtttcttgcc gtccaccccg ggccatgcca gtgtgtcctc tgggtccccc    906

ccaaaaatct ggtcattcaa ggatcccctc ccaaggctat gcttttctat aacttttaaa    966

taaaccttgg ggggtgaatg gaataaaaaa aaaaaaaaaa aaaaaa                  1012
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<210> 4

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Met Asn Leu Trp Leu Leu Ala Cys Leu Val Ala Gly Phe Leu Gly Ala
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Trp Ala Pro Ala Val His Thr Gln Gly Val Phe Glu Asp Cys Cys Leu
        -5              -1  1               5

Ala Tyr His Tyr Pro Ile Gly Trp Ala Val Leu Arg Arg Ala Trp Thr
10                  15                  20                  25
```

```
Tyr Arg Ile Gln Glu Val Ser Gly Ser Cys Asn Leu Pro Ala Ala Ile
                30                  35                  40

Phe Tyr Leu Pro Lys Arg His Arg Lys Val Cys Gly Asn Pro Lys Ser
            45                  50                  55

Arg Glu Val Gln Arg Ala Met Lys Leu Leu Asp Ala Arg Asn Lys Val
        60                  65                  70

Phe Ala Lys Leu His His Asn Met Gln Thr Phe Gln Ala Gly Pro His
    75                  80                  85

Ala Val Lys Lys Leu Ser Ser Gly Asn Ser Lys Leu Ser Ser Ser Lys
90                  95                  100                 105

Phe Ser Asn Pro Ile Ser Ser Ser Lys Arg Asn Val Ser Leu Leu Ile
                110                 115                 120

Ser Ala Asn Ser Gly Leu
            125
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Met Cys Cys Thr Lys Ser Leu Leu Leu Ala Ala Leu Met Ser Val Leu
    -25                 -20                 -15

cta ctc cac ctc tgc ggc gaa tca gaa gca gca agc aac ttt gac tgc       96
Leu Leu His Leu Cys Gly Glu Ser Glu Ala Ala Ser Asn Phe Asp Cys
-10                 -5              -1  1               5

tgt ctt gga tac aca gac cgt att ctt cat cct aaa ttt att gtg ggc      144
Cys Leu Gly Tyr Thr Asp Arg Ile Leu His Pro Lys Phe Ile Val Gly
            10                  15                  20

ttc aca cgg cag ctg gcc aat gaa ggc tgt gac atc aat gct atc atc      192
Phe Thr Arg Gln Leu Ala Asn Glu Gly Cys Asp Ile Asn Ala Ile Ile
        25                  30                  35

ttt cac aca aag aaa aag ttg tct gtg tgc gca aat cca aaa cag act      240
Phe His Thr Lys Lys Lys Leu Ser Val Cys Ala Asn Pro Lys Gln Thr
    40                  45                  50

tgg gtg aaa tat att gtg cgt ctc ctc agt aaa aaa gtc aag aac atg      288
Trp Val Lys Tyr Ile Val Arg Leu Leu Ser Lys Lys Val Lys Asn Met
55                  60                  65                  70

taaaaactgt ggcttttctg gaatggaatt ggacatagcc caagaacaga aagaaccttg    348

ctggggttgg aggtttcact tgcacatcat ggagggttta gtgcttatct aatttgtgcc    408

tcactggact tgtccaatta atgaagttga ttcatattgc atcatagttt gctttgttta    468

agcatcacat taaagttaaa ctgtatttta tgttatttat agctgtaggt tttctgtgtt    528

tagctattta atactaattt tccataagct attttggttt agtgcaaagt ataaaattat    588

atttgggggg gaataagatt atatggactt ttttgcaagc aacaagctat tttttaaaaa    648

aaactattta acattctttt gtttatattg ttttgtctcc taaattgttg taattgcatt    708

ataaaataag aaaaatatta ataagacaaa tattgaaaat aaagaaacaa aaagttaaaa    768

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa                                 801
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<211> 96

<212> PRT

<213> Homo sapiens

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Leu Leu His Leu Cys Gly Glu Ser Glu Ala Ala Ser Asn Phe Asp Cys
-10 -5 -1 1 5

Cys Leu Gly Tyr Thr Asp Arg Ile Leu His Pro Lys Phe Ile Val Gly
10 15 20

Phe Thr Arg Gln Leu Ala Asn Glu Gly Cys Asp Ile Asn Ala Ile Ile
25 30 35

Phe His Thr Lys Lys Lys Leu Ser Val Cys Ala Asn Pro Lys Gln Thr
40 45 50

Trp Val Lys Tyr Ile Val Arg Leu Leu Ser Lys Lys Val Lys Asn Met
55 60 65 70

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gcctgcctct gttcaccctc c atg gcc ctg cta ctg gcc ctc agc ctg ctg 171
Met Ala Leu Leu Leu Ala Leu Ser Leu Leu
1 5 10

gtt ctc tgg act tcc cca gcc cca act ctg agt ggc acc aat gat gct 219

```
Val Leu Trp Thr Ser Pro Ala Pro Thr Leu Ser Gly Thr Asn Asp Ala
                15                  20                  25

gaa gac tgc tgc ctg tct gtg acc cag aaa ccc atc cct ggg tac atc      267
Glu Asp Cys Cys Leu Ser Val Thr Gln Lys Pro Ile Pro Gly Tyr Ile
            30                  35                  40

gtg agg aac ttc cac tac ctt ctc atc aag gat ggc tgc agg gtg cct      315
Val Arg Asn Phe His Tyr Leu Leu Ile Lys Asp Gly Cys Arg Val Pro
        45                  50                  55

gct gta gtg ttc acc aca ctg agg ggc cgc cag ctc tgt gca ccc cca      363
Ala Val Val Phe Thr Thr Leu Arg Gly Arg Gln Leu Cys Ala Pro Pro
    60                  65                  70

gac cag ccc tgg gta gaa cgc atc atc cag aga ctg cag agg acc tca      411
Asp Gln Pro Trp Val Glu Arg Ile Ile Gln Arg Leu Gln Arg Thr Ser
75                  80                  85                  90

gcc aag atg aag cgc cgc agc agt taacctatga ccgtgcagag ggagcccgga     465
Ala Lys Met Lys Arg Arg Ser Ser
                95

gtccgagtca agcattgtga attattacct aacctgggga accgaggacc agaaggaagg    525

accaggcttc cagctcctct gcaccagacc tgaccagcca ggacagggcc tggggtgtgt    585

gtgagtgtga gtgtgagcga gagggtgagt gtggtctaga gtaaagctgc tccaccccca    645

gattgcaatg ctaccaataa agccgcctgg tgtttacaac taaaaaaaaa aaaa          699
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<210> 8

<211> 98

<212> PRT

<213> Homo sapiens

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Met Ala Leu Leu Leu Ala Leu Ser Leu Leu Val Leu Trp Thr Ser Pro
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Ala Pro Thr Leu Ser Gly Thr Asn Asp Ala Glu Asp Cys Cys Leu Ser
            20                  25                  30

Val Thr Gln Lys Pro Ile Pro Gly Tyr Ile Val Arg Asn Phe His Tyr
        35                  40                  45
```

```
Leu Leu Ile Lys Asp Gly Cys Arg Val Pro Ala Val Val Phe Thr Thr
    50                  55                  60

Leu Arg Gly Arg Gln Leu Cys Ala Pro Pro Asp Gln Pro Trp Val Glu
65                  70                  75                  80

Arg Ile Ile Gln Arg Leu Gln Arg Thr Ser Ala Lys Met Lys Arg Arg
                85                  90                  95

Ser Ser
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1               5                   10                  15

att act cag ttg att ctg aga tgt tac tgt gct cct tgc agg agg tca       96
Ile Thr Gln Leu Ile Leu Arg Cys Tyr Cys Ala Pro Cys Arg Arg Ser
            20                  25                  30

ggc agt tct cca ggc tat ttg tac cga att gcc tac tcc ttg atc tgt      144
Gly Ser Ser Pro Gly Tyr Leu Tyr Arg Ile Ala Tyr Ser Leu Ile Cys
        35                  40                  45

gtt ctt ggc ctc ctg ggg aat att ctg gtg gtg atc acc ttt gct ttt      192
Val Leu Gly Leu Leu Gly Asn Ile Leu Val Val Ile Thr Phe Ala Phe
    50                  55                  60

tat aag aag gcc agg tct atg aca gac gtc tat ctc ttg aac atg gcc      240
Tyr Lys Lys Ala Arg Ser Met Thr Asp Val Tyr Leu Leu Asn Met Ala
65                  70                  75                  80
```

```
att gca gac atc ctc ttt gtt ctt act ctc cca ttc tgg gca gtg agt      288
Ile Ala Asp Ile Leu Phe Val Leu Thr Leu Pro Phe Trp Ala Val Ser
                85                  90                  95

cat gcc act ggt gcg tgg gtt ttc agc aat gcc acg tgc aag ttg cta      336
His Ala Thr Gly Ala Trp Val Phe Ser Asn Ala Thr Cys Lys Leu Leu
            100                 105                 110

aaa ggc atc tat gcc atc aac ttt aac tgc ggg atg ctg ctc ctg act      384
Lys Gly Ile Tyr Ala Ile Asn Phe Asn Cys Gly Met Leu Leu Leu Thr
        115                 120                 125

tgc att agc atg gac cgg tac atc gcc att gta cag gcg act aag tca      432
Cys Ile Ser Met Asp Arg Tyr Ile Ala Ile Val Gln Ala Thr Lys Ser
    130                 135                 140

ttc cgg ctc cga tcc aga aca cta ccg cgc agc aaa atc atc tgc ctt      480
Phe Arg Leu Arg Ser Arg Thr Leu Pro Arg Ser Lys Ile Ile Cys Leu
145                 150                 155                 160

gtt gtg tgg ggg ctg tca gtc atc atc tcc agc tca act ttt gtc ttc      528
Val Val Trp Gly Leu Ser Val Ile Ile Ser Ser Ser Thr Phe Val Phe
                165                 170                 175

aac caa aaa tac aac acc caa ggc agc gat gtc tgt gaa ccc aag tac      576
Asn Gln Lys Tyr Asn Thr Gln Gly Ser Asp Val Cys Glu Pro Lys Tyr
            180                 185                 190

caa act gtc tcg gag ccc atc agg tgg aag ctg ctg atg ttg ggg ctt      624
Gln Thr Val Ser Glu Pro Ile Arg Trp Lys Leu Leu Met Leu Gly Leu
        195                 200                 205

gag cta ctc ttt ggt ttc ttt atc cct ttg atg ttc atg ata ttt tgt      672
Glu Leu Leu Phe Gly Phe Phe Ile Pro Leu Met Phe Met Ile Phe Cys
    210                 215                 220

tac acg ttc att gtc aaa acc ttg gtg caa gct cag aat tct aaa agg      720
Tyr Thr Phe Ile Val Lys Thr Leu Val Gln Ala Gln Asn Ser Lys Arg
225                 230                 235                 240

cac aaa gcc atc cgt gta atc ata gct gtg gtg ctt gtg ttt ctg gct      768
His Lys Ala Ile Arg Val Ile Ile Ala Val Val Leu Val Phe Leu Ala
                245                 250                 255

tgt cag att cct cat aac atg gtc ctg ctt gtg acg gct gct aat ttg      816
Cys Gln Ile Pro His Asn Met Val Leu Leu Val Thr Ala Ala Asn Leu
            260                 265                 270

ggt aaa atg aac cga tcc tgc cag agc gaa aag cta att ggc tat acg      864
Gly Lys Met Asn Arg Ser Cys Gln Ser Glu Lys Leu Ile Gly Tyr Thr
        275                 280                 285

aaa act gtc aca gaa gtc ctg gct ttc ctg cac tgc tgc ctg aac cct      912
Lys Thr Val Thr Glu Val Leu Ala Phe Leu His Cys Cys Leu Asn Pro
    290                 295                 300
```

```
gtg ctc tac gct ttt att ggg cag aag ttc aga aac tac ttt ctg aag      960
Val Leu Tyr Ala Phe Ile Gly Gln Lys Phe Arg Asn Tyr Phe Leu Lys
305                 310                 315                 320

atc ttg aag gac ctg tgg tgt gtg aga agg aag tac aag tcc tca ggc     1008
Ile Leu Lys Asp Leu Trp Cys Val Arg Arg Lys Tyr Lys Ser Ser Gly
                325                 330                 335

ttc tcc tgt gcc ggg agg tac tca gaa aac att tct cgg cag acc agt     1056
Phe Ser Cys Ala Gly Arg Tyr Ser Glu Asn Ile Ser Arg Gln Thr Ser
            340                 345                 350

gag acc gca gat aac gac aat gcg tcg tcc ttc act atg tgatagaaag      1105
Glu Thr Ala Asp Asn Asp Asn Ala Ser Ser Phe Thr Met
        355                 360                 365

ctgagtctcc ctaa                                                    1119
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<210> 10

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1               5                   10                  15

Ile Thr Gln Leu Ile Leu Arg Cys Tyr Cys Ala Pro Cys Arg Arg Ser
            20                  25                  30

Gly Ser Ser Pro Gly Tyr Leu Tyr Arg Ile Ala Tyr Ser Leu Ile Cys
        35                  40                  45

Val Leu Gly Leu Leu Gly Asn Ile Leu Val Val Ile Thr Phe Ala Phe
    50                  55                  60

Tyr Lys Lys Ala Arg Ser Met Thr Asp Val Tyr Leu Leu Asn Met Ala
65                  70                  75                  80

Ile Ala Asp Ile Leu Phe Val Leu Thr Leu Pro Phe Trp Ala Val Ser
                85                  90                  95
```

```
His Ala Thr Gly Ala Trp Val Phe Ser Asn Ala Thr Cys Lys Leu Leu
            100                 105                 110

Lys Gly Ile Tyr Ala Ile Asn Phe Asn Cys Gly Met Leu Leu Leu Thr
        115                 120                 125

Cys Ile Ser Met Asp Arg Tyr Ile Ala Ile Val Gln Ala Thr Lys Ser
    130                 135                 140

Phe Arg Leu Arg Ser Arg Thr Leu Pro Arg Ser Lys Ile Ile Cys Leu
145                 150                 155                 160

Val Val Trp Gly Leu Ser Val Ile Ile Ser Ser Ser Thr Phe Val Phe
                165                 170                 175

Asn Gln Lys Tyr Asn Thr Gln Gly Ser Asp Val Cys Glu Pro Lys Tyr
            180                 185                 190

Gln Thr Val Ser Glu Pro Ile Arg Trp Lys Leu Leu Met Leu Gly Leu
        195                 200                 205

Glu Leu Leu Phe Gly Phe Phe Ile Pro Leu Met Phe Met Ile Phe Cys
    210                 215                 220

Tyr Thr Phe Ile Val Lys Thr Leu Val Gln Ala Gln Asn Ser Lys Arg
225                 230                 235                 240

His Lys Ala Ile Arg Val Ile Ile Ala Val Val Leu Val Phe Leu Ala
                245                 250                 255

Cys Gln Ile Pro His Asn Met Val Leu Leu Val Thr Ala Ala Asn Leu
            260                 265                 270

Gly Lys Met Asn Arg Ser Cys Gln Ser Glu Lys Leu Ile Gly Tyr Thr
        275                 280                 285

Lys Thr Val Thr Glu Val Leu Ala Phe Leu His Cys Cys Leu Asn Pro
    290                 295                 300

Val Leu Tyr Ala Phe Ile Gly Gln Lys Phe Arg Asn Tyr Phe Leu Lys
305                 310                 315                 320
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```
Ile Leu Lys Asp Leu Trp Cys Val Arg Arg Lys Tyr Lys Ser Ser Gly
                325                 330                 335

Phe Ser Cys Ala Gly Arg Tyr Ser Glu Asn Ile Ser Arg Gln Thr Ser
            340                 345                 350

Glu Thr Ala Asp Asn Asp Asn Ala Ser Ser Phe Thr Met
        355                 360                 365
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gaggaagctg cttcgggggg tgagcaaact ttttaaaatg cagaaatt atg atc tac      57
                                                    Met Ile Tyr
                                                    1

acc cgt ttc tta aaa ggc agt ctg aag atg gcc aat tac acg ctg gca      105
Thr Arg Phe Leu Lys Gly Ser Leu Lys Met Ala Asn Tyr Thr Leu Ala
    5                   10                  15

cca gag gat gaa tat gat gtc ctc ata gaa ggt gaa ctg gag agc gat      153
Pro Glu Asp Glu Tyr Asp Val Leu Ile Glu Gly Glu Leu Glu Ser Asp
20                  25                  30                  35

gag gca gag caa tgt gac aag tat gac gcc cag gca ctc tca gcc cag      201
Glu Ala Glu Gln Cys Asp Lys Tyr Asp Ala Gln Ala Leu Ser Ala Gln
                40                  45                  50

ctg gtg cca tca ctc tgc tct gct gtg ttt gtg atc ggt gtc ctg gac      249
Leu Val Pro Ser Leu Cys Ser Ala Val Phe Val Ile Gly Val Leu Asp
            55                  60                  65

aat ctc ctg gtt gtg ctt atc ctg gta aaa tat aaa gga ctc aaa cgc      297
Asn Leu Leu Val Val Leu Ile Leu Val Lys Tyr Lys Gly Leu Lys Arg
        70                  75                  80
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```
gtg gaa aat atc tat ctt cta aac ttg gca gtt tct aac ttg tgt ttc      345
Val Glu Asn Ile Tyr Leu Leu Asn Leu Ala Val Ser Asn Leu Cys Phe
    85                  90                  95

ttg ctt acc ctg ccc ttc tgg gct cat gct ggg ggc gat ccc atg tgt      393
Leu Leu Thr Leu Pro Phe Trp Ala His Ala Gly Gly Asp Pro Met Cys
100                 105                 110                 115

aaa att ctc att gga ctg tac ttc gtg ggc ctg tac agt gag aca ttt      441
Lys Ile Leu Ile Gly Leu Tyr Phe Val Gly Leu Tyr Ser Glu Thr Phe
                120                 125                 130

ttc aat tgc ctt ctg act gtg caa agg tac cta gtg ttt ttg cac aag      489
Phe Asn Cys Leu Leu Thr Val Gln Arg Tyr Leu Val Phe Leu His Lys
            135                 140                 145

ggc aac ttt ttc tca gcc agg agg agg gtg ccc tgt ggc atc att aca      537
Gly Asn Phe Phe Ser Ala Arg Arg Arg Val Pro Cys Gly Ile Ile Thr
        150                 155                 160

agt gtc ctg gca tgg gta aca gcc att ctg gcc act ttg cct gaa ttc      585
Ser Val Leu Ala Trp Val Thr Ala Ile Leu Ala Thr Leu Pro Glu Phe
    165                 170                 175

gtg gtt tat aaa cct cag atg gaa gac cag aaa tac aag tgt gca ttt      633
Val Val Tyr Lys Pro Gln Met Glu Asp Gln Lys Tyr Lys Cys Ala Phe
180                 185                 190                 195

agc aga act ccc ttc ctg cca gct gat gag aca ttc tgg aag cat ttt      681
Ser Arg Thr Pro Phe Leu Pro Ala Asp Glu Thr Phe Trp Lys His Phe
                200                 205                 210

ctg act tta aaa atg aac att tcg gtt ctt gtc ctc ccc cta ttt att      729
Leu Thr Leu Lys Met Asn Ile Ser Val Leu Val Leu Pro Leu Phe Ile
            215                 220                 225

ttt aca ttt ctc tat gtg caa atg aga aaa aca cta agg ttc agg gag      777
Phe Thr Phe Leu Tyr Val Gln Met Arg Lys Thr Leu Arg Phe Arg Glu
        230                 235                 240

cag agg tat agc ctt ttc aag ctt gtt ttt gcc gta atg gta gtc ttc      825
Gln Arg Tyr Ser Leu Phe Lys Leu Val Phe Ala Val Met Val Val Phe
    245                 250                 255

ctt ctg atg tgg gcg ccc tac aat att gca ttt ttc ctg tcc act ttc      873
Leu Leu Met Trp Ala Pro Tyr Asn Ile Ala Phe Phe Leu Ser Thr Phe
260                 265                 270                 275

aaa gaa cac ttc tcc ctg agt gac tgc aag agc agc tac aat ctg gac      921
Lys Glu His Phe Ser Leu Ser Asp Cys Lys Ser Ser Tyr Asn Leu Asp
                280                 285                 290

aaa agt gtt cac atc act aaa ctc atc gcc acc acc cac tgc tgc atc      969
Lys Ser Val His Ile Thr Lys Leu Ile Ala Thr Thr His Cys Cys Ile
            295                 300                 305
```

```
aac cct ctc ctg tat gcg ttt ctt gat ggg aca ttt agc aaa tac ctc     1017
Asn Pro Leu Leu Tyr Ala Phe Leu Asp Gly Thr Phe Ser Lys Tyr Leu
        310                 315                 320

tgc cgc tgt ttc cat ctg cgt agt aac acc cca ctt caa ccc agg ggg     1065
Cys Arg Cys Phe His Leu Arg Ser Asn Thr Pro Leu Gln Pro Arg Gly
    325                 330                 335

cag tct gca caa ggc aca tcg agg gaa gaa cct gac cat tcc acc gaa     1113
Gln Ser Ala Gln Gly Thr Ser Arg Glu Glu Pro Asp His Ser Thr Glu
340                 345                 350                 355

gtg taaactagca tccaccaaat gcaagaagaa taaacatgga ttttcatctt          1166
Val

tctgcattat ttcatgtaaa ttttctacac atttgtatac aaaatcggat acaggaagaa   1226

aagggagagg tgagctaaca tttgctaagc actgaatttg tctcaggcac cgtgcaaggc   1286

tctttacaaa cgtgagctcc ttcgcctcct accacttgtc catagtgtgg ataggactag   1346

tctcatttct ctgagaagaa aactaaggcg cggaaatttg tctaagatca cataactagg   1406

aagtggcaga actgattctc cagccctggt agcatttgct cagagcctac gcttggtcca   1466

gaacatcaaa ctccaaaccc tggggacaaa cgacatgaaa taaatgtatt ttaaaacata   1526

taaaaaaaaa aaaaaaaaaa a                                             1547
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<210> 12

<211> 356

<212> PRT

<213> Homo sapiens

<400> 12

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Met Ile Tyr Thr Arg Phe Leu Lys Gly Ser Leu Lys Met Ala Asn Tyr
1               5                   10                  15

Thr Leu Ala Pro Glu Asp Glu Tyr Asp Val Leu Ile Glu Gly Glu Leu
            20                  25                  30

Glu Ser Asp Glu Ala Glu Gln Cys Asp Lys Tyr Asp Ala Gln Ala Leu
        35                  40                  45
```

```
Ser Ala Gln Leu Val Pro Ser Leu Cys Ser Ala Val Phe Val Ile Gly
    50                  55                  60

Val Leu Asp Asn Leu Leu Val Val Leu Ile Leu Val Lys Tyr Lys Gly
65                  70                  75                  80

Leu Lys Arg Val Glu Asn Ile Tyr Leu Leu Asn Leu Ala Val Ser Asn
                85                  90                  95

Leu Cys Phe Leu Leu Thr Leu Pro Phe Trp Ala His Ala Gly Gly Asp
            100                 105                 110

Pro Met Cys Lys Ile Leu Ile Gly Leu Tyr Phe Val Gly Leu Tyr Ser
        115                 120                 125

Glu Thr Phe Phe Asn Cys Leu Leu Thr Val Gln Arg Tyr Leu Val Phe
    130                 135                 140

Leu His Lys Gly Asn Phe Phe Ser Ala Arg Arg Arg Val Pro Cys Gly
145                 150                 155                 160

Ile Ile Thr Ser Val Leu Ala Trp Val Thr Ala Ile Leu Ala Thr Leu
                165                 170                 175

Pro Glu Phe Val Val Tyr Lys Pro Gln Met Glu Asp Gln Lys Tyr Lys
            180                 185                 190

Cys Ala Phe Ser Arg Thr Pro Phe Leu Pro Ala Asp Glu Thr Phe Trp
        195                 200                 205

Lys His Phe Leu Thr Leu Lys Met Asn Ile Ser Val Leu Val Leu Pro
    210                 215                 220

Leu Phe Ile Phe Thr Phe Leu Tyr Val Gln Met Arg Lys Thr Leu Arg
225                 230                 235                 240

Phe Arg Glu Gln Arg Tyr Ser Leu Phe Lys Leu Val Phe Ala Val Met
                245                 250                 255

Val Val Phe Leu Leu Met Trp Ala Pro Tyr Asn Ile Ala Phe Phe Leu
            260                 265                 270
```

Ser Thr Phe Lys Glu His Phe Ser Leu Ser Asp Cys Lys Ser Ser Tyr
275 280 285

Asn Leu Asp Lys Ser Val His Ile Thr Lys Leu Ile Ala Thr Thr His
290 295 300

Cys Cys Ile Asn Pro Leu Leu Tyr Ala Phe Leu Asp Gly Thr Phe Ser
305 310 315 320

Lys Tyr Leu Cys Arg Cys Phe His Leu Arg Ser Asn Thr Pro Leu Gln
325 330 335

Pro Arg Gly Gln Ser Ala Gln Gly Thr Ser Arg Glu Glu Pro Asp His
340 345 350

Ser Thr Glu Val
355

<210> 13

<211> 355

<212> PRT

<213> Homo sapiens

<400> 13

Met Glu Thr Pro Asn Thr Thr Glu Asp Tyr Asp Thr Thr Thr Glu Phe
1 5 10 15

Asp Tyr Gly Asp Ala Thr Pro Cys Gln Lys Val Asn Glu Arg Ala Phe
20 25 30

Gly Ala Gln Leu Leu Pro Pro Leu Tyr Ser Leu Val Phe Val Ile Gly
35 40 45

Leu Val Gly Asn Ile Leu Val Val Leu Val Leu Val Gln Tyr Lys Arg
50 55 60

Leu Lys Asn Met Thr Ser Ile Tyr Leu Leu Asn Leu Ala Ile Ser Asp
65 70 75 80

```
Leu Leu Phe Leu Phe Thr Leu Pro Phe Trp Ile Asp Tyr Lys Leu Lys
                85                  90                  95

Asp Asp Trp Val Phe Gly Asp Ala Met Cys Lys Ile Leu Ser Gly Phe
            100                 105                 110

Tyr Tyr Thr Gly Leu Tyr Ser Glu Ile Phe Phe Ile Ile Leu Leu Thr
        115                 120                 125

Ile Asp Arg Tyr Leu Ala Ile Val His Ala Val Phe Ala Leu Arg Ala
    130                 135                 140

Arg Thr Val Thr Phe Gly Val Ile Thr Ser Ile Ile Ile Trp Ala Leu
145                 150                 155                 160

Ala Ile Leu Ala Ser Met Pro Gly Leu Tyr Phe Ser Lys Thr Gln Trp
                165                 170                 175

Glu Phe Thr His His Thr Cys Ser Leu His Phe Pro His Glu Ser Leu
            180                 185                 190

Arg Glu Trp Lys Leu Phe Gln Ala Leu Lys Leu Asn Leu Phe Gly Leu
        195                 200                 205

Val Leu Pro Leu Leu Val Met Ile Ile Cys Tyr Thr Gly Ile Ile Lys
    210                 215                 220

Ile Leu Leu Arg Arg Pro Asn Glu Lys Lys Ser Lys Ala Val Arg Leu
225                 230                 235                 240

Ile Phe Val Ile Met Ile Ile Phe Phe Leu Phe Trp Thr Pro Tyr Asn
                245                 250                 255

Leu Thr Ile Leu Ile Ser Val Phe Gln Asp Phe Leu Phe Thr His Glu
            260                 265                 270

Cys Glu Gln Ser Arg His Leu Asp Leu Ala Val Gln Val Thr Glu Val
        275                 280                 285

Ile Ala Tyr Thr His Cys Cys Val Asn Pro Val Ile Tyr Ala Phe Val
    290                 295                 300
```

```
Gly Glu Arg Phe Arg Lys Tyr Leu Arg Gln Leu Phe His Arg Arg Val
305                 310                 315                 320

Ala Val His Leu Val Lys Trp Leu Pro Phe Leu Ser Val Asp Arg Leu
                325                 330                 335

Glu Arg Val Ser Ser Thr Ser Pro Ser Thr Gly Glu His Glu Leu Ser
            340                 345                 350

Ala Gly Phe
        355
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<210> 14

<211> 374

<212> PRT

<213> Homo sapiens

<400> 14

```
Met Leu Ser Thr Ser Arg Ser Arg Phe Ile Arg Asn Thr Asn Glu Ser
1               5                   10                  15

Gly Glu Glu Val Thr Thr Phe Phe Asp Tyr Asp Tyr Gly Ala Pro Cys
            20                  25                  30

His Lys Phe Asp Val Lys Gln Ile Gly Ala Gln Leu Leu Pro Pro Leu
        35                  40                  45

Tyr Ser Leu Val Phe Ile Phe Gly Phe Val Gly Asn Met Leu Val Val
    50                  55                  60

Leu Ile Leu Ile Asn Cys Lys Lys Leu Lys Cys Leu Thr Asp Ile Tyr
65                  70                  75                  80

Leu Leu Asn Leu Ala Ile Ser Asp Leu Leu Phe Leu Ile Thr Leu Pro
                85                  90                  95

Leu Trp Ala His Ser Ala Ala Asn Glu Trp Val Phe Gly Asn Ala Met
            100                 105                 110
```

```
Cys Lys Leu Phe Thr Gly Leu Tyr His Ile Gly Tyr Phe Gly Gly Ile
        115                 120                 125

Phe Phe Ile Ile Leu Leu Thr Ile Asp Arg Tyr Leu Ala Ile Val His
    130                 135                 140

Ala Val Phe Ala Leu Lys Ala Arg Thr Val Thr Phe Gly Val Val Thr
145                 150                 155                 160

Ser Val Ile Thr Trp Leu Val Ala Val Phe Ala Ser Val Pro Gly Ile
                165                 170                 175

Ile Phe Thr Lys Cys Gln Lys Glu Asp Ser Val Tyr Val Cys Gly Pro
            180                 185                 190

Tyr Phe Pro Arg Gly Trp Asn Asn Phe His Thr Ile Met Arg Asn Ile
        195                 200                 205

Leu Gly Leu Val Leu Pro Leu Leu Ile Met Val Ile Cys Tyr Ser Gly
    210                 215                 220

Ile Leu Lys Thr Leu Leu Arg Cys Arg Asn Glu Lys Lys Arg His Arg
225                 230                 235                 240

Ala Val Arg Val Ile Phe Thr Ile Met Ile Val Tyr Phe Leu Phe Trp
                245                 250                 255

Thr Pro Tyr Asn Ile Val Ile Leu Leu Asn Thr Phe Gln Glu Phe Phe
            260                 265                 270

Gly Leu Ser Asn Cys Glu Ser Thr Ser Gln Leu Asp Gln Ala Thr Gln
        275                 280                 285

Val Thr Glu Thr Leu Gly Met Thr His Cys Cys Ile Asn Pro Ile Ile
    290                 295                 300

Tyr Ala Phe Val Gly Glu Lys Phe Arg Ser Leu Phe His Ile Ala Leu
305                 310                 315                 320

Gly Cys Arg Ile Ala Pro Leu Gln Lys Pro Val Cys Gly Gly Pro Gly
                325                 330                 335
```

Val Arg Pro Gly Lys Asn Val Lys Val Thr Thr Gln Gly Leu Leu Asp
340 345 350

Gly Arg Gly Lys Gly Lys Ser Ile Gly Arg Ala Pro Glu Ala Ser Leu
355 360 365

Gln Asp Lys Glu Gly Ala
370

<210> 15

<211> 355

<212> PRT

<213> Homo sapiens

<400> 15

Met Thr Thr Ser Leu Asp Thr Val Glu Thr Phe Gly Thr Thr Ser Tyr
1 5 10 15

Tyr Asp Asp Val Gly Leu Leu Cys Glu Lys Ala Asp Thr Arg Ala Leu
20 25 30

Met Ala Gln Phe Val Pro Pro Leu Tyr Ser Leu Val Phe Thr Val Gly
35 40 45

Leu Leu Gly Asn Val Val Val Val Met Ile Leu Ile Lys Tyr Arg Arg
50 55 60

Leu Arg Ile Met Thr Asn Ile Tyr Leu Leu Asn Leu Ala Ile Ser Asp
65 70 75 80

Leu Leu Phe Leu Val Thr Leu Pro Phe Trp Ile His Tyr Val Arg Gly
85 90 95

His Asn Trp Val Phe Gly His Gly Met Cys Lys Leu Leu Ser Gly Phe
100 105 110

Tyr His Thr Gly Leu Tyr Ser Glu Ile Phe Phe Ile Ile Leu Leu Thr
115 120 125

```
Ile Asp Arg Tyr Leu Ala Ile Val His Ala Val Phe Ala Leu Arg Ala
    130                 135                 140

Arg Thr Val Thr Phe Gly Val Ile Thr Ser Ile Val Thr Trp Gly Leu
145                 150                 155                 160

Ala Val Leu Ala Ala Leu Pro Glu Phe Ile Phe Tyr Glu Thr Glu Glu
                165                 170                 175

Leu Phe Glu Glu Thr Leu Cys Ser Ala Leu Tyr Pro Glu Asp Thr Val
            180                 185                 190

Tyr Ser Trp Arg His Phe His Thr Leu Arg Met Thr Ile Phe Cys Leu
        195                 200                 205

Val Leu Pro Leu Leu Val Met Ala Ile Cys Tyr Thr Gly Ile Ile Lys
    210                 215                 220

Thr Leu Leu Arg Cys Pro Ser Lys Lys Lys Tyr Lys Ala Ile Arg Leu
225                 230                 235                 240

Ile Phe Val Ile Met Ala Val Phe Phe Ile Phe Trp Thr Pro Tyr Asn
                245                 250                 255

Val Ala Ile Leu Leu Ser Ser Tyr Gln Ser Ile Leu Phe Gly Asn Asp
            260                 265                 270

Cys Glu Arg Ser Lys His Leu Asp Leu Val Met Leu Val Thr Glu Val
        275                 280                 285

Ile Ala Tyr Ser His Cys Cys Met Asn Pro Val Ile Tyr Ala Phe Val
    290                 295                 300

Gly Glu Arg Phe Arg Lys Tyr Leu Arg His Phe Phe His Arg His Leu
305                 310                 315                 320

Leu Met His Leu Gly Arg Tyr Ile Pro Phe Leu Pro Ser Glu Lys Leu
                325                 330                 335

Glu Arg Thr Ser Ser Val Ser Pro Ser Thr Ala Glu Pro Glu Leu Ser
            340                 345                 350
```

Ile Val Phe
355

<210> 16

<211> 360

<212> PRT

<213> Homo sapiens

<400> 16

Met Asn Pro Thr Asp Ile Ala Asp Thr Thr Leu Asp Glu Ser Ile Tyr
1 5 10 15

Ser Asn Tyr Tyr Leu Tyr Glu Ser Ile Pro Lys Pro Cys Thr Lys Glu
20 25 30

Gly Ile Lys Ala Phe Gly Glu Leu Phe Leu Pro Pro Leu Tyr Ser Leu
35 40 45

Val Phe Val Phe Gly Leu Leu Gly Asn Ser Val Val Val Leu Val Leu
50 55 60

Phe Lys Tyr Lys Arg Leu Arg Ser Met Thr Asp Val Tyr Leu Leu Asn
65 70 75 80

Leu Ala Ile Ser Asp Leu Leu Phe Val Phe Ser Leu Pro Phe Trp Gly
85 90 95

Tyr Tyr Ala Ala Asp Gln Trp Val Phe Gly Leu Gly Leu Cys Lys Met
100 105 110

Ile Ser Trp Met Tyr Leu Val Gly Phe Tyr Ser Gly Ile Phe Phe Val
115 120 125

Met Leu Met Ser Ile Asp Arg Tyr Leu Ala Ile Val His Ala Val Phe
130 135 140

Ser Leu Arg Ala Arg Thr Leu Thr Tyr Gly Val Ile Thr Ser Leu Ala
145 150 155 160

```
Thr Trp Ser Val Ala Val Phe Ala Ser Leu Pro Gly Phe Leu Phe Ser
                165                 170                 175

Thr Cys Tyr Thr Glu Arg Asn His Thr Tyr Cys Lys Thr Lys Tyr Ser
            180                 185                 190

Leu Asn Ser Thr Thr Trp Lys Val Leu Ser Ser Leu Glu Ile Asn Ile
        195                 200                 205

Leu Gly Leu Val Ile Pro Leu Gly Ile Met Leu Phe Cys Tyr Ser Met
    210                 215                 220

Ile Ile Arg Thr Leu Gln His Cys Lys Asn Glu Lys Lys Asn Lys Ala
225                 230                 235                 240

Val Lys Met Ile Phe Ala Val Val Val Leu Phe Leu Gly Phe Trp Thr
                245                 250                 255

Pro Tyr Asn Ile Val Leu Phe Leu Glu Thr Leu Val Glu Leu Glu Val
            260                 265                 270

Leu Gln Asp Cys Thr Phe Glu Arg Tyr Leu Asp Tyr Ala Ile Gln Ala
        275                 280                 285

Thr Glu Thr Leu Ala Phe Val His Cys Cys Leu Asn Pro Ile Ile Tyr
    290                 295                 300

Phe Phe Leu Gly Glu Lys Phe Arg Lys Tyr Ile Leu Gln Leu Phe Lys
305                 310                 315                 320

Thr Cys Arg Gly Leu Phe Val Leu Cys Gln Tyr Cys Gly Leu Leu Gln
                325                 330                 335

Ile Tyr Ser Ala Asp Thr Pro Ser Ser Ser Tyr Thr Gln Ser Thr Met
            340                 345                 350

Asp His Asp Leu His Asp Ala Leu
        355                 360
```

<210> 17

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> HPRT sense primer

<400> 17
gtaatgatca gtcaacgggg gac 23

<210> 18

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> HPRT antisense primer

<400> 18
ccagcaagct tgcaaccttа acca 24

<210> 19

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> FLAG epitope tag sequence

<400> 19

Asp Tyr Lys Asp Asp Asp Asp Lys Leu
1 5

<210> 20

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> TECK sense primer

<400> 20
ccttcaggta tctggagagg agatc 25

<210> 21

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> TECK antisense primer

<400> 21
cacgcttgta ctgttggggt tc 22

<210> 22

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> exon 1-specific CRAM primer

<400> 22
agacgcttca gagatcctct ggaggcc 27

<210> 23

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> exon 2-specific CRAM primer

<400> 23
gaagctgctt cgggggggtga gcaaac 26

<210> 24

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> exon 3-specific CRAM primer

<400> 24
caaacacagc agagcagagt gatggcacc 29

<210> 25

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> CRAM primer

<400> 25
gtgtcctggc atgggtaaca gcc 23

<210> 26

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> CRAM primer

<400> 26
cggtggaatg gtcaggttct tccc 24